Validated By CRFValidator v 1.0.2

Application No: 10566929 Version No: 1.0

Input Set:

Output Set:

Started: 2007-05-30 14:29:02.006
Finished: 2007-05-30 14:29:05.064
Elapsed: 0 hr(s) 0 min(s) 3 sec(s) 58 ms
Total Warnings: 16
Total Errors: 0
No. of SeqIDs Defined: 24
Actual SeqID Count: 24

Error code		Error Description
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SEQUENCE LISTING

<110> Yang, Meija

<120> NOVEL THERAPEUTIC FUSION PROTEINS

<130> ARS-121

<140> 10566929
<141> 2007-05-30

<150> US 10/566,929
<151> 2006-02-02

<150> US 60/492,397
<151> 2003-08-04

<160> 24

<170> PatentIn version 3.1

<210> 1

<211> 183

<212> PRT

<213> Homo sapiens

<400> 1

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Arg Leu Leu Arg Ser His Ser Leu His Tyr Leu Phe Met Gly Ala Ser
1               5                  10                  15

Glu Gln Asp Leu Gly Leu Ser Leu Phe Glu Ala Leu Gly Tyr Val Asp
            20                  25                  30

Asp Gln Leu Phe Val Phe Tyr Asp His Glu Ser Arg Arg Val Glu Pro
        35                  40                  45

Arg Thr Pro Trp Val Ser Ser Arg Ile Ser Ser Gln Met Trp Leu Gln
    50                  55                  60

Leu Ser Gln Ser Leu Lys Gly Trp Asp His Met Phe Thr Val Asp Phe
65                  70                  75                  80
```

```
Trp Thr Ile Met Glu Asn His Asn His Ser Lys Glu Ser His Thr Leu
                85                  90                  95

Gln Val Ile Leu Gly Cys Glu Met Gln Glu Asp Asn Ser Thr Glu Gly
            100                 105                 110

Tyr Trp Lys Tyr Gly Tyr Asp Gly Gln Asp His Leu Glu Phe Cys Pro
        115                 120                 125

Asp Thr Leu Asp Trp Arg Ala Ala Glu Pro Arg Ala Trp Pro Thr Lys
    130                 135                 140

Leu Glu Trp Glu Arg His Lys Ile Arg Ala Arg Gln Asn Arg Ala Tyr
145                 150                 155                 160

Leu Glu Arg Asp Cys Pro Ala Gln Leu Gln Gln Leu Leu Glu Leu Gly
                165                 170                 175

Arg Gly Val Leu Asp Gln Gln
            180
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<210> 2

<211> 661

<212> PRT

<213> Homo sapiens

<400> 2

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Gly Pro Pro Val Ser Cys Ile Lys Arg Asp Ser Pro Ile Gln Cys Ile
1               5                   10                  15

Gln Ala Ile Ala Glu Asn Arg Ala Asp Ala Val Thr Leu Asp Gly Gly
            20                  25                  30

Phe Ile Tyr Glu Ala Gly Leu Ala Pro Tyr Lys Leu Arg Pro Val Ala
        35                  40                  45

Ala Glu Val Tyr Gly Thr Glu Arg Gln Pro Arg Thr His Tyr Tyr Ala
    50                  55                  60

Val Ala Val Val Lys Lys Gly Gly Ser Phe Gln Leu Asn Glu Leu Gln
65                  70                  75                  80

Gly Leu Lys Ser Cys His Thr Gly Leu Arg Arg Thr Ala Gly Trp Asn
                85                  90                  95

Val Pro Ile Gly Thr Leu Arg Pro Phe Leu Asn Trp Thr Gly Pro Pro
            100                 105                 110

Glu Pro Ile Glu Ala Ala Val Ala Arg Phe Phe Ser Ala Ser Cys Val
        115                 120                 125
```

```
Pro Gly Ala Asp Lys Gly Gln Phe Pro Asn Leu Cys Arg Leu Cys Ala
    130                 135                 140

Gly Thr Gly Glu Asn Lys Cys Ala Phe Ser Ser Gln Glu Pro Tyr Phe
145                 150                 155                 160

Ser Tyr Ser Gly Ala Phe Lys Cys Leu Arg Asp Gly Ala Gly Asp Val
                165                 170                 175

Ala Phe Ile Arg Glu Ser Thr Val Phe Glu Asp Leu Ser Asp Glu Ala
            180                 185                 190

Glu Arg Asp Glu Tyr Glu Leu Leu Cys Pro Asp Asn Thr Arg Lys Pro
        195                 200                 205

Val Asp Lys Phe Lys Asp Cys His Leu Ala Arg Val Pro Ser His Ala
    210                 215                 220

Val Val Ala Arg Ser Val Asn Gly Lys Glu Asp Ala Ile Trp Asn Leu
225                 230                 235                 240

Leu Arg Gln Ala Gln Glu Lys Phe Gly Lys Asp Lys Ser Pro Lys Phe
                245                 250                 255

Gln Leu Phe Gly Ser Pro Ser Gly Gln Lys Asp Leu Leu Phe Lys Asp
            260                 265                 270

Ser Ala Ile Gly Phe Ser Arg Val Pro Pro Arg Ile Asp Ser Gly Leu
        275                 280                 285

Tyr Leu Gly Ser Gly Tyr Phe Thr Ala Ile Gln Asn Leu Arg Lys Ser
    290                 295                 300

Glu Glu Glu Val Ala Ala Arg Arg Ala Arg Val Val Trp Cys Ala Val
305                 310                 315                 320

Gly Glu Gln Glu Leu Arg Lys Cys Asn Gln Trp Ser Gly Leu Ser Glu
                325                 330                 335

Gly Ser Val Thr Cys Ser Ser Ala Ser Thr Thr Glu Asp Cys Ile Ala
            340                 345                 350

Leu Val Leu Lys Gly Glu Ala Asp Ala Met Ser Leu Asp Gly Gly Tyr
        355                 360                 365

Val Tyr Thr Ala Gly Lys Cys Gly Leu Val Pro Val Leu Ala Glu Asn
    370                 375                 380

Tyr Lys Ser Gln Gln Ser Ser Asp Pro Asp Pro Asn Cys Val Asp Arg
385                 390                 395                 400

Pro Val Glu Gly Tyr Leu Ala Val Ala Val Val Arg Arg Ser Asp Thr
                405                 410                 415

Ser Leu Thr Trp Asn Ser Val Lys Gly Lys Lys Ser Cys His Thr Ala
            420                 425                 430
```

```
Val Asp Arg Thr Ala Gly Trp Asn Ile Pro Met Gly Leu Leu Phe Asn
        435                 440                 445

Gln Thr Gly Ser Cys Lys Phe Asp Glu Tyr Phe Ser Gln Ser Cys Ala
    450                 455                 460

Pro Gly Ser Asp Pro Arg Ser Asn Leu Cys Ala Leu Cys Ile Gly Asp
465                 470                 475                 480

Glu Gln Gly Glu Asn Lys Cys Val Pro Asn Ser Asn Glu Arg Tyr Tyr
                485                 490                 495

Gly Tyr Thr Gly Ala Phe Arg Cys Leu Ala Glu Asn Ala Gly Asp Val
            500                 505                 510

Ala Phe Val Lys Asp Val Thr Val Leu Gln Asn Thr Asp Gly Asn Asn
        515                 520                 525

Asn Glu Ala Trp Ala Lys Asp Leu Lys Leu Ala Asp Phe Ala Leu Leu
    530                 535                 540

Cys Leu Asp Gly Lys Arg Lys Pro Val Thr Glu Ala Arg Ser Cys His
545                 550                 555                 560

Leu Ala Met Ala Pro Asn His Ala Val Val Ser Arg Met Asp Lys Val
                565                 570                 575

Glu Arg Leu Lys Gln Val Leu Leu His Gln Gln Ala Lys Phe Gly Arg
            580                 585                 590

Asn Gly Ser Asp Cys Pro Asp Lys Phe Cys Leu Phe Gln Ser Glu Thr
        595                 600                 605

Lys Asn Leu Leu Phe Asn Asp Asn Thr Glu Cys Leu Ala Arg Leu His
    610                 615                 620

Gly Lys Thr Thr Tyr Glu Lys Tyr Leu Gly Pro Gln Tyr Val Ala Gly
625                 630                 635                 640

Ile Thr Asn Leu Lys Lys Cys Ser Thr Ser Pro Leu Leu Glu Ala Cys
                645                 650                 655

Glu Phe Leu Arg Lys
            660
```

<210> 3

<211> 92

<212> PRT

<213> Homo sapiens

<400> 3

Val Pro Pro Leu Val Lys Val Thr His His Val Thr Ser Ser Val Thr
1 5 10 15

Thr Leu Arg Cys Arg Ala Leu Asn Tyr Tyr Pro Gln Asn Ile Thr Met
20 25 30

Lys Trp Leu Lys Asp Lys Gln Pro Met Asp Ala Lys Glu Phe Glu Pro
35 40 45

Lys Asp Val Leu Pro Asn Gly Asp Gly Thr Tyr Gln Gly Trp Ile Thr
50 55 60

Leu Ala Val Pro Pro Gly Glu Glu Gln Arg Tyr Thr Cys Gln Val Glu
65 70 75 80

His Pro Gly Leu Asp Gln Pro Leu Ile Val Ile Trp
85 90

<210> 4

<211> 753

<212> PRT

<213> Artificial sequence

<220>
<223> Lactoferin / HFE-based recycling domain RC1

<400> 4

Gly Pro Pro Val Ser Cys Ile Lys Arg Asp Ser Pro Ile Gln Cys Ile
1 5 10 15

Gln Ala Ile Ala Glu Asn Arg Ala Asp Ala Val Thr Leu Asp Gly Gly
20 25 30

Phe Ile Tyr Glu Ala Gly Leu Ala Pro Tyr Lys Leu Arg Pro Val Ala
35 40 45

Ala Glu Val Tyr Gly Thr Glu Arg Gln Pro Arg Thr His Tyr Tyr Ala
50 55 60

Val Ala Val Val Lys Lys Gly Gly Ser Phe Gln Leu Asn Glu Leu Gln
65 70 75 80

Gly Leu Lys Ser Cys His Thr Gly Leu Arg Arg Thr Ala Gly Trp Asn
85 90 95

Val Pro Ile Gly Thr Leu Arg Pro Phe Leu Asn Trp Thr Gly Pro Pro
100 105 110

```
Glu Pro Ile Glu Ala Ala Val Ala Arg Phe Phe Ser Ala Ser Cys Val
        115                 120                 125

Pro Gly Ala Asp Lys Gly Gln Phe Pro Asn Leu Cys Arg Leu Cys Ala
    130                 135                 140

Gly Thr Gly Glu Asn Lys Cys Ala Phe Ser Ser Gln Glu Pro Tyr Phe
145                 150                 155                 160

Ser Tyr Ser Gly Ala Phe Lys Cys Leu Arg Asp Gly Ala Gly Asp Val
                165                 170                 175

Ala Phe Ile Arg Glu Ser Thr Val Phe Glu Asp Leu Ser Asp Glu Ala
            180                 185                 190

Glu Arg Asp Glu Tyr Glu Leu Leu Cys Pro Asp Asn Thr Arg Lys Pro
        195                 200                 205

Val Asp Lys Phe Lys Asp Cys His Leu Ala Arg Val Pro Ser His Ala
    210                 215                 220

Val Val Ala Arg Ser Val Asn Gly Lys Glu Asp Ala Ile Trp Asn Leu
225                 230                 235                 240

Leu Arg Gln Ala Gln Glu Lys Phe Gly Lys Asp Lys Ser Pro Lys Phe
                245                 250                 255

Gln Leu Phe Gly Ser Pro Ser Gly Gln Lys Asp Leu Leu Phe Lys Asp
            260                 265                 270

Ser Ala Ile Gly Phe Ser Arg Val Pro Pro Arg Ile Asp Ser Gly Leu
        275                 280                 285

Tyr Leu Gly Ser Gly Tyr Phe Thr Ala Ile Gln Asn Leu Arg Lys Ser
    290                 295                 300

Glu Glu Glu Val Ala Ala Arg Arg Ala Arg Val Val Trp Cys Ala Val
305                 310                 315                 320

Gly Glu Gln Glu Leu Arg Lys Cys Asn Gln Trp Ser Gly Leu Ser Glu
                325                 330                 335

Gly Ser Val Thr Cys Ser Ser Ala Ser Thr Thr Glu Asp Cys Ile Ala
            340                 345                 350

Leu Val Leu Lys Gly Glu Ala Asp Ala Met Ser Leu Asp Gly Gly Tyr
        355                 360                 365

Val Tyr Thr Ala Gly Lys Cys Gly Leu Val Pro Val Leu Ala Glu Asn
    370                 375                 380

Tyr Lys Ser Gln Gln Ser Ser Asp Pro Asp Pro Asn Cys Val Asp Arg
385                 390                 395                 400

Pro Val Glu Gly Tyr Leu Ala Val Ala Val Val Arg Arg Ser Asp Thr
                405                 410                 415
```

```
Ser Leu Thr Trp Asn Ser Val Lys Gly Lys Lys Ser Cys His Thr Ala
            420                 425                 430

Val Asp Arg Thr Ala Gly Trp Asn Ile Pro Met Gly Leu Leu Phe Asn
        435                 440                 445

Gln Thr Gly Ser Cys Lys Phe Asp Glu Tyr Phe Ser Gln Ser Cys Ala
    450                 455                 460

Pro Gly Ser Asp Pro Arg Ser Asn Leu Cys Ala Leu Cys Ile Gly Asp
465                 470                 475                 480

Glu Gln Gly Glu Asn Lys Cys Val Pro Asn Ser Asn Glu Arg Tyr Tyr
                485                 490                 495

Gly Tyr Thr Gly Ala Phe Arg Cys Leu Ala Glu Asn Ala Gly Asp Val
            500                 505                 510

Ala Phe Val Lys Asp Val Thr Val Leu Gln Asn Thr Asp Gly Asn Asn
        515                 520                 525

Asn Glu Ala Trp Ala Lys Asp Leu Lys Leu Ala Asp Phe Ala Leu Leu
    530                 535                 540

Cys Leu Asp Gly Lys Arg Lys Pro Val Thr Glu Ala Arg Ser Cys His
545                 550                 555                 560

Leu Ala Met Ala Pro Asn His Ala Val Val Ser Arg Met Asp Lys Val
                565                 570                 575

Glu Arg Leu Lys Gln Val Leu Leu His Gln Gln Ala Lys Phe Gly Arg
            580                 585                 590

Asn Gly Ser Asp Cys Pro Asp Lys Phe Cys Leu Phe Gln Ser Glu Thr
        595                 600                 605

Lys Asn Leu Leu Phe Asn Asp Asn Thr Glu Cys Leu Ala Arg Leu His
    610                 615                 620

Gly Lys Thr Thr Tyr Glu Lys Tyr Leu Gly Pro Gln Tyr Val Ala Gly
625                 630                 635                 640

Ile Thr Asn Leu Lys Lys Cys Ser Thr Ser Pro Leu Leu Glu Ala Cys
                645                 650                 655

Glu Phe Leu Arg Lys Val Pro Pro Leu Val Lys Val Thr His His Val
            660                 665                 670

Thr Ser Ser Val Thr Thr Leu Arg Cys Arg Ala Leu Asn Tyr Tyr Pro
        675                 680                 685

Gln Asn Ile Thr Met Lys Trp Leu Lys Asp Lys Gln Pro Met Asp Ala
    690                 695                 700

Lys Glu Phe Glu Pro Lys Asp Val Leu Pro Asn Gly Asp Gly Thr Tyr
705                 710                 715                 720
```

```
Gln Gly Trp Ile Thr Leu Ala Val Pro Pro Gly Glu Glu Gln Arg Tyr
                725                 730                 735

Thr Cys Gln Val Glu His Pro Gly Leu Asp Gln Pro Leu Ile Val Ile
            740                 745                 750

Trp
```

<210> 5

<211> 275

<212> PRT

<213> Artificial sequence

<220>
<223> Lactoferin / HFE-based recycling domain RC2

<400> 5

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1               5                   10                  15

Glu Gln Asp Leu Gly Leu Ser Leu Phe Glu Ala Leu Gly Tyr Val Asp
            20                  25                  30

Asp Gln Leu Phe Val Phe Tyr Asp His Glu Ser Arg Arg Val Glu Pro
        35                  40                  45

Arg Thr Pro Trp Val Ser Ser Arg Ile Ser Ser Gln Met Trp Leu Gln
    50                  55                  60

Leu Ser Gln Ser Leu Lys Gly Trp Asp His Met Phe Thr Val Asp Phe
65                  70                  75                  80

Trp Thr Ile Met Glu Asn His Asn His Ser Lys Glu Ser His Thr Leu
                85                  90                  95

Gln Val Ile Leu Gly Cys Glu Met Gln Glu Asp Asn Ser Thr Glu Gly
            100                 105                 110

Tyr Trp Lys Tyr Gly Tyr Asp Gly Gln Asp His Leu Glu Phe Cys Pro
        115                 120                 125

Asp Thr Leu Asp Trp Arg Ala Ala Glu Pro Arg Ala Trp Pro Thr Lys
    130                 135                 140

Leu Glu Trp Glu Arg His Lys Ile Arg Ala Arg Gln Asn Arg Ala Tyr
145                 150                 155                 160

Leu Glu Arg Asp Cys Pro Ala Gln Leu Gln Gln Leu Leu Glu Leu Gly
                165                 170                 175
```

```
Arg Gly Val Leu Asp Gln Gln Val Pro Pro Leu Val Lys Val Thr His
            180                 185                 190

His Val Thr Ser Ser Val Thr Thr Leu Arg Cys Arg Ala Leu Asn Tyr
        195                 200                 205

Tyr Pro Gln Asn Ile Thr Met Lys Trp Leu Lys Asp Lys Gln Pro Met
    210                 215                 220

Asp Ala Lys Glu Phe Glu Pro Lys Asp Val Leu Pro Asn Gly Asp Gly
225                 230                 235                 240

Thr Tyr Gln Gly Trp Ile Thr Leu Ala Val Pro Pro Gly Glu Glu Gln
                245                 250                 255

Arg Tyr Thr Cys Gln Val Glu His Pro Gly Leu Asp Gln Pro Leu Ile
            260                 265                 270

Val Ile Trp
        275
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<210> 6

<211> 753

<212> PRT

<213> Artificial sequence

<220>
<223> Lactoferin / HFE-based recycling domain RC3

<400> 6

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Val Pro Pro Leu Val Lys Val Thr His His Val Thr Ser Ser Val Thr
1               5                   10                  15

Thr Leu Arg Cys Arg Ala Leu Asn Tyr Tyr Pro Gln Asn Ile Thr Met
            20                  25                  30
```